IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

MAY 1 2 2003

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In re the application of: Curtis, Rory A.J/

Serial No.: 09/587,111

Filed: June 2, 2000

For: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID RECEPTOR FAMILY OF

PROTEINS AND USES THEREOF

Attorney Docket No.: MNI-062CP2DV1

Commissioner for Patents

Box AF

Washington, D.C. 20231

Group Art Unit: 1646

Examiner: Ulm, J. D.

Certificate of Facsimile Transmission

I hereby certify that this correspondence is being facsimile transmitted to the Commissioner for Patents, Box AF, Washington, D.C. 20231 on the date set forth below.

By:

Date of Signature

María Laccotripe Zacharakis, Ph.D.

Attorney for Applicant

Limited Recognition Under 37 C.F.R. 10.9(b)

DECLARATION PURSUANT TO 37 CFR §1.131

Dear Sir:

I, Rory A.J. Curtis, a citizen of the United Kingdom, residing at 78 Hardwick Road,

Ashland, Massachusetts 01721 hereby declare as follows:

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- (1) I am the inventor of the subject matter described and claimed in the above-identified application.
- (2) Prior to January 22, 1999, the invention described and claimed in the abovereferenced patent application was completed in this country, as evidenced by the following:
- (a) Prior to January 22, 1999 I had completed the sequencing of the full length human VR-2 (SEQ ID NO:5) as evidenced by copies of the assembled contig map and the complete sequence of SEQ ID NO:5 derived from the contig map. The contig map and sequence print-out are submitted herewith as Exhibits A and B, respectively.
- (b) Prior to January 22, 1999 I had determined that the polypeptide of SEQ ID NO:5 was a vanilloid receptor based on the results of a blast search using the amino acid sequence of SEQ ID NO:5. The top hit in this blast search analysis is rat vanilloid receptor 1 (VR-1; accession number AF029310). Based on the percent identity and percent similarity between the polypeptide of SEQ ID NO:5 and rat VR-1, and the fact that rat VR-1 was the top hit in the blast search analysis I determined that the polypeptide of SEQ ID NO:5 was a vanilloid receptor. The results of the blast search analysis are submitted herewith as Exhibit C.
- (c) Prior to January 22, 1999, I had determined that the polypeptide of SEQ ID NO:5 represents a unique target for pain and that it may be responsible for hypersensitivity in chronic neuropathic pain, as evidenced by a copy of the "Qualified Target Summary Sheet" generated for this molecule. The Qualified Target Summary Sheet is submitted herewith as Exhibit D.

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(d) According to my routine practice, immediately after identifying the polypeptide of SEQ ID NO:5 as a vanilloid receptor (hVR-2) associated with pain and classifying it as a Qualified Target, I contemplated routine uses of this molecule such as: (i) use of the molecule in screening assays to identify modulators of the vanilloid receptor or (ii) use of this molecule in the diagnosis of conditions/diseases associated with, for example, aberrant vanilloid receptor (hVR-2) nucleic acid expression or activity, e.g., pain disorders, as evidenced by a copy of the "Qualified Target Summary Sheet" generated for this molecule.

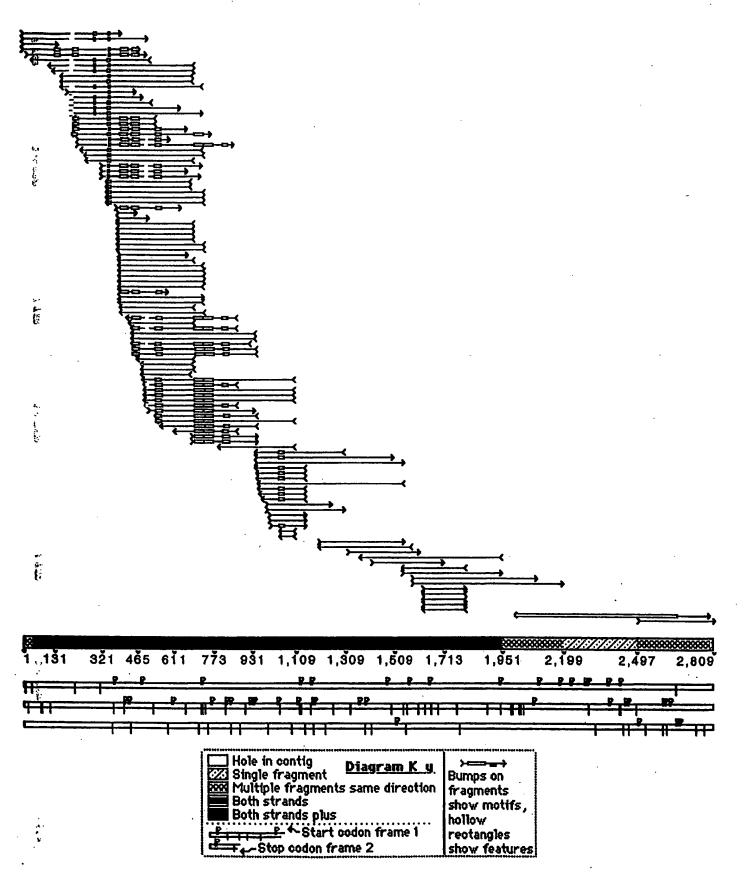
(e) The dates deleted from the contig map (Exhibit A), the sequence print-out (Exhibit B), the blast search results (Exhibit C), and the Qualified Target Summary (Exhibit D) are prior to January 22, 1999.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this Application for Patent or any patent issuing thereon.

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21e11a Sequencher™ "21e11racefinal"



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21ella Sequencher** "21ellracefinal"

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2 flbx21e11r18a2 067
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2 flb:21e11r17a1 #63
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21hx21ellr15a1 #63
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£11bx21e11r15a2 #62
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Elbx1ellx18al #62 GATTTTGGGA GCGGGCTGCC TCCCATGGAG TCACAGTTCC AGGGCGAGGA CCGGAAATTC GCCCCTCAGA TAAGAGTCAA CCTCAACTAC
A Elbx21011x1602 861 GATTTGGGA GCGGGCTGCC TCCCATGGAG TCACAGTTCC AGGGCGAGGA CCGGAAATTC GCCCCTCAGA TAAGAGTCAA CCTCAACTAC
2 F1bx21el1rr13_ 660 GATTTGGGA GCGGGCTGCC TCCCATGGAG TCACAGTTCC AGGGCGAGGA CCGGAAATTC GCCCCTCAGA TAAGAGTCAA CCTCAACTAC
£1bx21e11r17v1 #60
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  Genbank AA74... §32
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                                                                                         CTCAGA TAAGAGTCAA CCTCAACTAC
Elbx21e11r22g1 #21 GATTTGGGA GCGGGCTGCC TCCCATGGAG TCACAGTTCC AGGGCGAGGA CCGGAAATTC GCCCCTCAGA TAAGAGTCAA CCTCAACTAC
  Genbank AA768... #9 GATTTTGGGA GCGGGCTGCC TCCCATGGAG TCACAGTTCC AGGGCGAGGA CCGGAAATT
                                                                                         CTCAGA TAAGAGTCAA CCTCAACTAC
🔁 £1hx11e11r19a2 | 48 GATTINGGAA GCGGGCTGCC TCCCATGAAG TCNCAGTTCA AGGGCGAGGA CCGGAAATTC GCCCCTCAGA TAAGAGTCAA CCTCAACTAC
A Elbx21611x1961 68 GATTTGGGA GCGGGCTGCC TCCCATGAAG TCACAGTTCC AGGGCGAGGA CCGGAAATTC GCCCCTCAGA TAAGAGTCAA CTTCAACTAC
Gerbank Aliza. 16 GATTTTGGGA GCGGGCTGCC TCCCATGGAG TCACAGTTCC AGGGCGAGGA CCGGAAATT
                                                                                         CTCAGA TANGAGTCAA CCTCAACTAC
Sithaloseva 13 Gattingga negggetgee teceatgnag teacagttee agggegagga engnaaatte geeceteaga taagagteaa eeteaactae
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21ella Sequencher** "21ellracefinal"

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		TTTGGGA	GCGGWC TGCW	1CCCATGBIAG	TCACAGTTCC	MOGNEGAGGA	CCGMAAATTC	GCCCNTCAGA	TAAGAGTCAC	CCTCAACTAC
Sth21011r18			TGCC	TCCCATGGAG	TCACAGTTCC	AGGGCGAGGA	CCGGAAATTC	GCCCCTCAGA	TAAGAGTCAA	CCTCAACTAC
A £110021-011-721				AG	TCACAGTTCC	AGGNCGAGGA	CCGGRAATTC	GCCCTCAGA	TAAGAGTCAA	CCTCAACTAC
2 Clbx21011r17				AG	TCACAGTTCC	AGGGCGAGGA	CCGGAAATTC	GCCCCTCAGA	TAAGAGTCAA	CCTCAACTAC
Stinx31e11x35"					TCACAGTTCC	AGGGCGAGGN	CCGGAAATTC	GCCCCTCAGA	TAAGAGTCAA	CCTCAACTAC
2 £18021e11rr1				,	TCC	A: GGCGAGGN	CGGAAATTTC	NCCCNTCAGA	TARARGTCAC	CCTCAACTNC
Genbank AA4						AGGGCGAGGA	CCGGAAATT	CTCAGA	TAAGAGTCAA	CCTCAACTAC
flbx21e11rr1						AGGNCGAAGA	CCGGAAATTC	GCCCNTCAGA	TAAGAGTCAC	CNTCANCTIC
flhx21e11rrl						GGGCGAGGA	CCGGAAATTN	GCCCNTCAGA	TAAGAGTCAA	CCTCAACTAC
flhx2le11rrl						GGC : AGG :	NCGGAAATTC	GCCCTCAAA	TAA: AGTCAA	CCTCAACTNC
Gembank AA8						GGA	CCGGAAATT	CTCAGA	TAAGAGTCAA	CCTCAACTAC
Genbank AA2							TC	GCCCCTCAGA	TAAGAGTCAA	CCTCAACTAC
🗿 jthsa103e2w1	>11>									TAC
								······································		***************************************

#451 GATTTTGGGA GCGGGCTGCC TCCCATGGAG TCACAGTTCC AGGGCGAGGA CCGGAAATTC GCCCCTCAGA TAAGAGTCAA CCTCAACTAC D F G S G L P P M E S Q F Q G E D R K F A P Q I R V N L N Y

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21ella Sequencher "21ellracefinal"

flbxc21e1		# 400									
flhxc21el	igz	#428	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	r ccaaaccgat	TTGACCGAGA	TCGGCTCTNC	AATGCGGTCT	CCCGGGGTG	CCCCGAGGAT
21hx21011	-do rAt	#410	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	r ccaaaccgat	TTGACCGAGA	TCGGCTCHNC	AATGCGGTCT	CCCGGGGTG	CCCCGAGGAT
flbx1e11	-2.0	#380	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGA	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTG	CCCCGAGGAT
flhxc21e1	114 114	#380	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGA1	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
flhxc21e1	IN)	4360	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTG	CCCCGAGGAT
flhxc21e1	TD1	#340	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTNCCCGAGA	TCGGCTCTTN	ATTGCGGGCT	CCGGGGGTGT	CCCNAAGGAT
jthsa103e	102	#340	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTNTTT	AATGCGGGCT	CCCGGGGTGT	CCCGAAGGAT
jtheal03e	4b2	9332	CGAAAGGGA	•							
CIBALU36	(DI	#332	CGAAAGGGA								
jthsa103e2	162	#332	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	TADDADOO:
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_				CAGGTGCCAG							
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flhx21e11x	21	#286	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCARACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
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Genbank H			CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCNAGGAT
Genbank H			CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCARACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
Gembank H			CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
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flbx21e11r	20	#2 02	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
flhx21e11r	22	\$ 202	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
flbx21e11r	22	\$ 202	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
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£lbk2lei1r	16	157	CGARAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCARACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	СССОВОСТОТ	CCCCGAGGAI
flhx21e11r			CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGANNAM
£lbi21e11r			CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCORNAN
Elbx21e11r			CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGGTGT	CCCTGAGGAT
fibuleilr	2 0 :	157	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCARACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGGTGT	CCCCGAGGAT
flhx21e11r	18	1 157	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
Supprison 1 a			CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	NCCGGGGGTGT	CCCCGAGGAT
flhxllellr	17	1153	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGGTGT	CCCCGAGGAT
filhElellr	17	153	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	TADDADOOO
[Click lettr	15	#153	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	СССВВВВТВТ	CCCTGAGGAT
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flbx21e11r		150		CAGGTGCCAG					AATGCGGTCT	CCCGGGGGGGG	000000000
fibolelin		1150	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
flhxClellr:	16 (1149	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGGGG	CCCCARCOS
fib:clelir	16 (149	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGGGGG	CCCCGAGGAT
Genbank A		1132	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGGGG	CCCCGACGGAT
Elbiziellr:		1111	CGAAAGGGAA	CAGGTGCCAG	NCAGCCGGAT	CCAAACCGAT	TTGACCNAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGGGG	CCCCANGGAT
Genbank A		#99	CGARAGGGAA	CAGATGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGGGGG	CCCCANGGAT
flhx2le11r		#98	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGGTCT	CCCGGGGGGG	CCCCGAGGAT
Elpx31e11xi	19a1	198	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGCGGTCT	CCCCCCCCCCC	CCCCGAGGAT
Genbenk A	12	#96	AADGDAAADO	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AATGOCGOCO	CCCGGGGTGT	CCCCTAGGAT
jthsa103e2v	a .	₽ 93	CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCAAACCGAT	TTGACCGAGA	TCGGCTCTTC	AAROOGGEGG	CCCGGGGTGT	CCCCGAGGAT
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filmbleilri	18g1		CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCARACCGAM	TROBOCONON	ACGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
Elbizieiir:	1g1		CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAM	CCARACCOAT	TORCOGRAN	TOGGCTUTTC	AATGCGGTCT	CCGGGGTGT	CCCCGAGGAT
Elbizieliri	7g1		CGAAAGGGAA	CAGGTGCCAG	TCAGCCGGAT	CCARACCOAT	MENDAGO CO	TCUGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGNAT
Element 12	12g2		CHARAGGGAA	CAGGTGCCAG	TCACCCCCA	CCARACCOAT	MICACCOAGA	TOUGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGAGGAT
2 sibizielira	12.,	# 54	CGAAA: GGAA	CAGGTCCCAG	TCAGCGGGAA	CORRECCIO	ENGROCCIAGA	TCGGCTCTTC	AATGCGGTCT	CCCGGGGTGT	CCCCGANGAT
Genbank A	46	#51	CGAAAGGGAA	CAGGTGCCAG	TCAGCCCCAR	TABUUNAANU	MECACCUAUA	TOOGGETTTC	AATCGGTTCT	CCGGGGGGTGT	CCCCGAGGAT
2 flbx2lellrr	13_	# 51	CGAAAAGGAA	DACCOTOROAC	TCACCCCCC	CANADONA	TIGACCGAGA	TCGGCTCTTC	AATGCGGTCT (CCCGGGGTGT	CCCCGAGGAT
flhzlellr:			MGAAAGGAA	CAGGTCCCAG	TODOCCUST	OO. BANG	TANCHGAGA	TCGG:TTTTC	AATCGGGTCT (CNGGGGTGT	CCCCGAGGAT
				CAGGTGCCAG	- CA : NCGGAT	CCIAANC AT	ADADOOADT	TCGGCTCTTC	AATCGGTTCT (CCGGGGGTGT	CCCNGAGGAT

21ella Sequencher "21ellracefinal"

Ċ	\$ 541	CGAAAG	IGGAI	A C	AGGTG	CCA	G 9	CAG	cce	GAT	CCI	AAA	CCGA	 r 1	TTGACCG	AGA	TCG	CTC	TTC	ААТ	aca	GTC	T	CCCGG	GGTG	T (cccc	GAGG	
Genbank AIO	>#1>																					c	T	ccce	GGTG	T (cccc	GAGG	7AT
1thsa103e2x2						CA	G :	rcag	cca	GAT	CCI	AAA	CCGA	rı	TGACCG	AGA	TCG	3CTC	TTC	λAT	GCG	GTC	T	ccca	GTG	T (ćccc	GAGG	JAT
2 flbx21e11rr9		AAAA													PTGACCG														
jthsa103e2w1	84		GGA	A C	AGGTO	CCA	G :	rcag	CCG	GAT	CCI	AAA	CCGA	r 2	PTGACCG	AGA	TCG	3CTC	TTC	AAT	GCG	GTC	T	ccca	GGTG	T (cccc	GAGG	3AT
Genbank AA23.	- #33	CGAAAG	IG: A	A C	AGGT	CCA	G :	rcag	CCG	GAT	CCI	AAA	CCGA:	r 7	TGACCO	AGA	TCG	3CTC	TTC	AAT	GCG	GTC	T	ccca	GGTG	r	CCC:	GAGG	JAT
ed compatik wert	- #44	CGAAAG	HOGA	A C	AGGTG	ICCA(G 7	rcag	CCC	GAT	CC1	NAA(CCGA:	T 7	PDDARDT	AGA	TCGC	CTC	TTC	AAT	aca	GTC	ጥ .	CCC . C	ACC TO	100	CCCC	4000	330
elleniololleria	. #49	COAAAG	GGA	4 C	AGGT	CCA	: :	AADI	CCG	GAT	CC	AAA	CCGA	r 1	rtgaccg	AGA	TIG)GT1	TTC	AAT	CGG	GTC	T	ccca	GGTG	T	cccc	GAGG	TAE

21e11a Sequencher "21e11racefinal"

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A finacioligi $500 ctggctggac ttccagagta cctgagcaag accagcaagt acctcaccga ctcggaatac acagagggnt cca
A flbx21e11x19_ 4470 CTGGCTGGAC TTCCAGAGTA CCTGAGCAAG ACCAGCAAGT ACCTCACCGN CTCGGAAT: C NCAGAGGG
A firmibilitis. 1470 CTGGCTGGAC TTCCAGAGTA CCTGAGCAAG ACCAGCAAGT ACCTCACCGA CTCGGAATAC ACAGAGGGG
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Aflhxc21e11b2 4430
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🔁 jth8a103a2t2 | 1422 | CTGGCTGGAC TTNCAGAGTA CCTGAGCAAG ANCAGCAAGT
A jthmal03e2t1 1421 CTGGCTGGAC TTCCAGAGTA CCTGAGCAAG ACCAGCAAGT ACCTCACCGA CTCGGAATAC ACAGANGGCT MCACANGTAA GACGTGCCTG
Sithmalo3e02L. 1410 CTGGCTGGAC TTCCAGAGTA CCTGAGCAAG ACCAGCAAGT ACCTCACCGA CTCGGAATAC ACAGAGGGCT CCACAGGTAA GACGTGCCTG
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🙎 Gembank H49... #310 CTGGCTGGAC TTCCAGAGTA CCTGAGCAAG ACCAGCAAGT ACCTCACCGA CTTGGAATAC ACAGAGGGGT CCACAGGTAA GACGTGCCTG
A f1bx21e11r20_ 4292 CTGGCTGGAC TTCCAGAGTA CCTGAGCAAG ACCAGCAAGT ACCTCNCCGA CTCGGAA
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A fibrielizi6... 1247 CTGGCTGGAC TTCCAGAGTA CCTGAGCAAG ACCAGCAAGT ACCTCACCGA CTCGGAATAC ACAGA
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A fibx21e11r15_ 1247 CTGGCTGGAC TTCCAGAGTA CCTGAGCAAG ACCAGCAAGT ACCTCACCGA CTCGGAATAC NCAGAG
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M K A V L N L K D G V N A C I L P L L Q I D R D S G N P O P

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A fibrile 1271 - $501 CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCACCAG CCTGCAGGCC
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finoc12c4b3... #313 GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTTTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
 Genbank AA9... #279 GCCGCCAAGG AGGGCAAGAT CGAGATCTTC AGGCACATCC T
🚧 jtma029c10t1... 167 GCCGCCAAGO AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCOAG
Genbank W386... 165 GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTNTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
                                                                        TTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
Genbank AA3... >#1>
            $1261 GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTTTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
                  AARE GRIEIF RHIL QRE FSG LSHL SRK FTE
🛃 frhob012c04s... 1411 TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCT:G CTTCTGTGGA CAGCTGTGAG GAGAACTCAA TGCTGGAGAT CATTGCCTTT
 finoclicand... 4403 Tegreciate egectetee egeteteete tateacetee etteteteea caeetetea eagaactea tectegabat cattecett
Sthla029clot. 1157 TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTGTGGA CAGCTGTGAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
  Genbank W38. 4155 TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTGTGGA CAGCTGTGAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
   Genbank AA35... $38 TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTNTGGA CAGCTGTNAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
                            GGCCTGTNCG GGTGTCNCTG TATGACNTGG CTTCTGTGNA CAGCTGTGAN GAGAACTCAG TGCTGGAGAT CATTGCCTTT
frtob12c4c1... >#1>
Genbank N24... >#1>
                                                                                GAGAACTCAG TGCTGGAGAT CATTGNCTTT
            #1351 TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTGTGGA CAGCTGTGAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
                              PVR VSL YDLASVD SCE ENSV LEI IAF
                   WCYG
2 1thob012c04s_ 4501 CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGNTTTGG AGCCCCTGAA CAAACTGCTG C
🕰 1:hob012:048... 1501 CATTGCAAGA ACCCGCACCG ACACCGAATG GTCGNTTTGG AGCCCCTGAA CAAACTGCTG CANGCGAAAT GGGATCTGCT CAT:CCCAAG
A ithoc1204h3... 1493 CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGN AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAA
Sithle029clot. 1247 Cattgcaaga gcccgnaccg acaccgaatg gtcgttttgg agcccctgaa caaactgctg cangcgaaat gggatctgct catnchcaag
Gendank M38. 1245 CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
Gendenk AA3... $128 CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
ETADD120401.4... #81 CATTGCAAGA GNCCGCACCG ACACNGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGNCGAAAT GGGATCTGCT CATCCCCAAG
   Genbank N242. #31 CATTGCAAGA GCCCGNACCG ACACCGAATG GTCGTTTTGG AGCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
             $1441 CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
                   R C K S P H R H R M V V L B P L N K L L Q A K W D L L I P K
```

21e11a Sequencher "21e11racefinal"

Achrh21e11 #425 Exhob12c4d1 >#1>	GGCACTAAG	CAGATGGCAG	CCCGGATGAG	CGCTGGTGCT	TCAGGGTGGA	GGAGGTGAAC		GGGAGCAGAC GGGAGCAGAC	
#2431	GGCACTAAGG				TCAGGGTGGA F R V E			GGGAGCAGAC W E Q T	GCTGCCTACG L P T
Achrh21e11 #515 2 frhob12c4d1.a #25									
#2521	CTGTGTGAG			CCTCGAACTC P R T		TGTCCTGGCT V L A	TCCCCTCCCA	AGGAGGATGA K E D E	GGATGGTGCC D G A
Achrh21e11 \$605								AGGACAGAGC	
#2611	TCTGAGGAA. S E B				ACTGATGGCC N W P			AGGACAGAGC BDRA	
Achrb21e11 #695								AAAAAAAA A	
\$2701	TCCAACCAC S N H			AGTGAATTCT S B F	GGTGGCAAAT W W Q I		ACTAACTCAA T N S		**************************************
2 frhob12c4d1 #295	**************************************	A AAAAAAAA.							
#2791		A AAAAAAAAA K K K							

```
BLASTP vs. PNU (AA) flh21ellorfaa - 5:26:57 pm on Dec 21 98
BLASTP 1.4.10MP-WashU [30-Aug-96] (Build 20:24:58 Oct 21 1996]
Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers,
and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol.
215:403-10.
Query= flh21e11orfaa
        (764 letters)
           /disk0/asap/databases/db/NRP/protxnu
           345,099 sequences; 106,000,184 total letters.
Searching......done
                                                                    Smallest
                                                                      Sum
                                                             High
                                                                   Probability
Sequences producing High-scoring Segment Pairs:
                                                            Score
                                                                   P(N)
                                                                   1.9e-221
                                                              336
                                                                             7
GP:gi 2570933 (AF029310) vanilloid receptor subtype 1 [Ra...
GPU:gi | 3986159 | gpl | PID | d1035925 (AB015231) VR1sk [Mus mus...
                                                                   9.8e-136
                                                              299
                                                                             6
GP:gi 2911863 (AF047660) contains similarity to ankyrin r...
                                                              103
                                                                   6.5e-20
                                                                             8
GP:gi|3675319|gml|PID|e1344970 (Z74030) similar to ankyri...
                                                                             7
                                                               97
                                                                   1.1e-19
GP:gi 2642590 (AF031408) olfactory channel [Caenorhabditi...
                                                               93
                                                                   3.6e-16
                                                                             6
GP:gi 2854148 (AF045639) contains similarity to ankyrin r...
                                                               93
                                                                  4.1e-16
GP:gi 3879753 gnl PID e1349345 (Z72514) Similarity to Hum...
                                                                   3.6e-11
                                                               73
GP:gi 3287188 gnl PID e315126 (Y10601) ankyrin-like prote...
                                                               71
                                                                   2.7e-08
SP:SP:SP P48994 TRPL_DROME TRANSIENT-RECEPTOR-POTENTIAL L...
                                                                69
                                                                   2.2e-05
                                                                             4
                                                                   5.6e-05
GP:gi|1841966 (U65916) ankyrin [Rattus norvegicus]
                                                               72
          Descriptions of 4 database sequences were not reported due to the
WARNING:
          limiting value of parameter V = 1.
>GP:gi|2570933 (AF029310) vanilloid receptor subtype 1 [Rattus norvegicus]
            Length = 838
 Score = 336 (156.0 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221
 Identities = 67/112 (59%), Positives = 84/112 (75%)
         206 FYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHALVMISDNSAENIAL 265
Query:
             FYFGELPLSLAACT Q +V +LL+N QPA + A DS GNTVLHALV ++DN+ +N
         245 FYFGELPLSLAACTNQLAIVKFLLQNSWQPADISARDSVGNTVLHALVEVADNTVDNTKF 304
Sbjct:
         266 VTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAAKEGKIEIFRHILQRE 317
Query:
             VTSMY+ +L GA+L PT++LE+1 N + LTPL LAA GKI + +ILQRE
         305 VTSMYNEILILGAKLHPTLKLEEITNRKGLTPLALAASSGKIGVLAYILQRE 356
Sbjct:
 Score = 316 (146.7 bits), Expect = 1.9e-22%. Sum P(7) = 1.9e-221
 Identities = 65/138 (47%), Positives = 93/138 (67%)
          66 ASQPDPNRFDRDRLFNAVSRGVPEDLAGLPHYLSKTSKYLTDSEYTEGSTGKTCLMKAVL 125
Query:
                                   ++L L +L ++ K LTDSE+ + TGKTCL+KA+L
             A + P +DR +F+AV++
         104 AGEKPPRLYDRRSIFDAVAQSNCQELESLLPFLQRSKKRLTDSEFKDPETGKTCLLKAML 163
Sbjct:
         126 NLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQÇVKLLVEN 185
Query:
             NL +G N I LL + R + + + VNA TD YY+G +ALHIAIE+R++ | V LLVEN
         164 NLHNGQNDTIALLLDVARKTDSLKQFVNAS!TDSYYKGQTALHIAIERRNMTLVTLLVEN 223
Sbjct:
         186 GANVHARACGRFFQKGQG 203
Query:
```

GA+V A A G FF+K +G

Sbjct: 224 GADVQAAANGDFFKKTKG 241

Score = 299 (138.8 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221 Identities = 69/175 (39%), Positives = 94/175 (53%)

Query: 391 FFLNFLCNLIYMFIFTAVAYHQPTLKKAAPHLKAEVGNSMLLTGHILILLGGTYLLVGQL 450

F+ NF +YM IFTA AY++P LK VG+ +TG IL +

Sbjct: 434 FYFNFFVYCLYMIIFTAAAYYRPVEGLPPYKLKNTVGDYFRVTGEILSVXXXXXXXRGI 493

Query: 451 WYFWRRHVFIWISFIDSYFEILFLFQALLKPVSQVLCFLAIEWYLPLLVSALPLGWLNLL 510

YF +R + F+DSY EILF Q+L VS VL F + Y+ +V +L +GW N+L

Sbjct: 494 QYFLQRRPSLKSLFVDSYSEILFFVQSLF1:LVSVVLYFSQRKEYVASMVFSLAMGWTNML 553

Query: 511 YYTRGFQHTGIYSVMIQKVILRDLLRFLLTYLVFLFGFAVALVSLSQEAWRPEAP 565

YYTRGFQ GIY+VMI+K+ILRDL R A+V+L ++ P
Sbjct: 554 YYTRGFQQMGIYAVMIEKMILRDLCRXXXXXXXXXXXXXXXXXXTAVVTLIEDGKNNSLP 608

Score = 281 (130.5 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221

Identities = 54/95 (56%), Positives = 70/95 (73%)

Query: 586 GAQYRGILEASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLNMLIALMS 645

G Y + LELFKFTIGMG+L F E F+ + ++LLLAYV+LTYILLLNMLIALM

Sbjct: 624 GNSYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVFIILLLAYVILTYILLLNMLIALMG 683

Query: 646 ETVNSVATDSWSIWKLQKAISVLEMENGYWWCRKK 680

ETVN +A +S +IWKLQ+AI++L+ E + C +K

Sbjct: 684 ETVNKIAQESKNIWKLQRAITILDTEKSFLKCMRK 718

Score = 162 (75.2 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221

Identities = 28/38 (73%), Positives = 34/33 (89%)

Query: 323 HLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360

HLSRKFTEW YGPV SLYDL+ +D+CE+NSVLE+IA+

Sbjct: 364 HLSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVIAY 401

Score = 144 (66.9 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221

Identities = 25/47 (53%), Positives = 31/47 (65%)

Query: 678 RKKORAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEOTLPTLCEDP 724

RK R+G +L VG PDG D RWCFRV+EVNW +W + + EDP

Sbjct: 717 RKAFRSGKLLQVGFTPDGKDDYRWCFRVDEVNWTTWNTNVGIINEDP 763

Score = 94 (43.6 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221

Identities = 15/30 (50%), Positives = 24/30 (80%)

Query: 363 KSPHRHRMVVLEPLNKLLQAKWDLLIPKFF 392

++P+RH M+++EPLN+LLQ KWD + + F

Sbjct: 405 ETPNRHDMLLVEFLNRLLQDKWDRFVKRIF 434

Score = 46 (21.4 bits), Expect = 1.3e-162, Sum P(6) = 1.3e-162

Identities = 11/48 (22%), Positives = 24/43 (50%)

Query: 435 HILILLGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQALLKPV 482

H ++L+ + L+ W +++F+F+ + I+F A +PV

Sbjct: 410 HDMLLVEPLNRLLQDKWDRFVKRIFYFNFFVYCLYMIIFTAAAYYRPV 457

Score = 37 (17.2 bits), Expect = 2.4e-169, Sum P(7) = 2.4e-169

Identities = 8/22 (36%), Positives = 13/22 (59%)

Query: 297 PLKLAAKEGKIEIFRHILQREF 318

PL LAA ++ I + +LQ +

Sbjct: 251 PLSLAACTNQLAIVKFLLQNSW 272

Score = 37 (17.2 bits), Expect = 1.9e-111, Sum P(7) = 1.9e-111Identities = 8/26 (30%), Positives = 15/26 (57%) 206 FYFGELPLSLAACTKQWDVVSYLLEN 231 Query: +Y G+ L +A + +V+ L+EN 198 YYKGQTALHIAIERRNMTLVTLLVEN 223 Sbjct: >GPU:gi|3986159|gnl|PID|d1035925 (AB015231) VRlsk [Mus musculus] Length = 563 Score = 299 (138.8 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136 Identities = 69/175 (39%), Positives = 94/175 (53%) 391 FFLNFLCNLIYMFIFTAVAYHQPTLKKAAPHLKAEVGNSMLLTGHILILLGGIYLLVGQL 450 +TG IL + +YM IFTA AY++P LK VG+ F+ NF 127 FYFNFFVYCLYMIIFTAAAYYRPVEGLPPYKLKNTVGDYFRVTGEILSVXXXXXXXRGI 186 Sbjct: 451 WYFWRRHUFIWISFIDSYFEILFLFQALLKPVSQVLCFLAIEWYLPLLVSALVLGWLNLL 510 Query: VS VL F + Y+ +V +L +GW N+L F+DSY EILF Q+L + 187 QYFLQRRPSLKSLFVDSYSEILFFVQSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNML 246 Sbjct: 511 YYTRGFOHTGIYSVMIQKVILRDLLRFLLIYLVFLFGFAVALVSLSQEAWRPEAP 565 Query: YYTRGFO GIY+VMI+K+ILRDL R A+V+L ++ 247 YYTRGFQQMGIYAVMIEKMILRDLCRXXXXXXXXXXXXXXXTAVVTLIEDGKNNSLP 301 Sbjct: Score = 253 (117.5 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136 Identities = 50/89 (56%). Positives = 64/89 (71%) 586 GAQYRGILEASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMS 645 Ouerv: LELFKFTIGMG+L F E F+ + ++LLLAYV+LTYILLLNMLIALM 317 GNSYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVFIILLLAYVILTYILLLNMLIALMG 376 Sbjat: 646 ETVNSVATDSWSIWKLQKAISVLEMENGY 674 Query: ETV V+ +S IWKLQ A ++L++E + 377 ETVGQVSKESKHIWKLQWATTILDIERSF 405 Sbjet: Score = 163 (75.7 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136Identities = 28/47 (59%), Positives = 34/47 (72%) 678 RKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTLPTLCEDP 724 Query: DG+PD RWCFRV+EVNW+ W Q L + EDP RK R+G M+TVG 410 RKAFRSGEMVTVGKSSDGTPDRRWCFRVDEVNWSHWNQNLGIINEDP 456 Sbjct: Score = 162 (75.2 bits), Expect = 9.8e-136, Sum P(6) = <math>9.8e-136Identities = 28/38 (73%), Positives = 34/3 (89%) Query: 323 HLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF - 360 HLSRKFTEW YGPV SLYDL+ +D+CE+NSVLE+LA+ 57 HLSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVIAY 94 Sbict: Score = 129 (59.9 birs), Expect = 9.8e-136, Sum P(6) = 9.8e-136Identities = 27/49 (55%), Positives = 36/49 (73%) 269 MYDGLLQAGARLCPTVQLEDIRMLQDLTPLKLAAKEGKIEIFRHILQRE 317 Query: MY+ +L GA+L PT++LE+I N + LTPL LAA GKI + +ILQRE 1 MYNEILILGAKLHPTLKLEEITNRKGLTPLALAASSGKIGVLAYILQRE 49 Sbjct:

Score = 94 (43.6 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136

Identities = 15/30 (50%), Positives = 24/30 (80%)

Query: 363 KSPHRHRMVVLEPLNKLLQAKWDLLIPKFF 392

++P+RH M+++EPLN+LLQ KWD + + F

Sbjct: 98 ETPNRHDMLLVEPLNRLLQDKWDRFVKRII 127

Score = 46 (21.4 bits), Expect = 2.3e-77, Sum P(5) = 2.3e-77 Identities = 11/48 (22%), Positives = 24/48 (50%)

Query: 435 HILILLGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQALLKPV 482 H ++L+ + L+ W + + +F + F+ + I+F A +PV

103 HDMLLVEPLNRLLQDKWDRFVKRIFYFNFFVYCLYMIIFTAAAYYRPV 150

Score = 42 (19.5 bits), Expect = 1.2e-122, Sum P(6) = 1.2e-122 Identities = 9/22 (40%), Positives = 16/22 (72%)

Query: 209 GELPLSLAACTKQWDVVSYLLE 230
G PL+LAA + + V++Y+L+
Sbjct: 26 GLTPLALAASSGKIGVLAYILQ 47

Sbjct:

>GP:gi|2911863 (AF047660) contains similarity to ankyrin repeats

[Caenorhabditis elegans]

Length = 900

Score = 103 (47.8 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20Identities = 23/89 (25%), Positives = 44/39 (49%)

Query: 497 LLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGFAVALVSLS 556 L+ ++ ++ LYY R + G + +M+ +I D+ RF+LIY +FL GF+ + +

Sbjct: 592 LITVTMIFTTVHYLYYCRVIRFVGPFVLMVYTIIATDIFRFMLIYGIFLMGFSQSFSLIF 651

Query: 557 QEAWRPEAPTGPNATESVQPMEGQEDEGN 585 R T+ + EG +++ N Sbjct: 652 LSCEREANVIKKLITDQSEASEGSDNKFN 680

Score = 63 (29.3 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20 Identities = 15/27 (55%), Positives = 18/27 (66%)

Query: 291 NLQDLTPLKLAAKEGKIEIFRHILQRE 317 N Q L+PL LAAK K E+F IL+ E Sbjct: 328 NKQSLSPLTLAAKLAKKEMFDEILELE 354

Score = 56 (26.0 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20 Identities = 16/48 (33%), Positives = 25/48 (52%)

Query: 151 LVNAQCTDDYYRGHSALHIAIEKRSLQCVkLLVENGANVHARACGRFF 198 L+N + + G S LH AI + V ++ GA+V++R G FF Sbjct: 185 LLNDIHISEDFYGLSPLHQAIINTDCKLVYKFLKLGADVNSRCYGAFF 232

Score = 54 (25.1 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20 Identities = 12/23 (52%), Positives = 13/23 (56%)

Query: 207 YFGELPLSLAACTKQWDVVSYLL 229 Y GE PLS AAC Q + LL Sbjct: 263 YLGEYPLSFAACLNQPESFRLLL 285

Score = 49 (22.8 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20Identities = 8/23 (34%), Positives = 12/23 (52%)

Query: 331 WCYGPVRVSLYDLASVDSCEENS 353 W YG + Y LA +D+ E + Sbjct: 359 WAYGDASSTAYPLAKIDTINETT 381

Score = 47 (21.8 bits), Expect = 6.5e-20, Aum P(8) = 6.5e-20 Identities = 11/30 (36%), Positives = 18/30 (60%)

Query: 236 ASLQATDSQGNTVLHALVMISDNSAENIAL 265
A+ A D+ GN+VLH V+ + + +AL

Sbjct: 289 ANPNAQDTNGNSVLHMCVIHENMAMFKLAL 318

Score = 46 (21.4 bits), Expect = 5.7e-13, Sum P(6) = 5.7e-13Identities = 9/27 (33%), Positives = 17/27 (62%)

Query: 163 GHSALHIAIEKRSLQCVKLLVENGANV 189
G+S LH+ + ++ KL +E GA++
Sbjct: 298 GNSVLHMCVIHENMAMFKLALECGASL 324

Score = 43 (20.0 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20Identities = 8/18 (44%), Positives = 13/18 (72%)

Query: 634 ILLINMLIALMSETVNSV 651 I+ NMLIA+M+ T ++

Sbjct: 753 IMOFNMLIAMMTRTYETI 770

Score = 41 (19.0 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20 Identities = 10/27 (37%), Positives = 16/27 (59%)

Query: 113 GSTGKTCLMKAVLNLKDGVNACILFLL 139
GS G+T + +L+ D NA +L +L
Sbjct: 153 GSMGETIIGCCLLHASDIHNALVLKIL 179

Score = 35 (16.3 bits), Expect = 0.00016, Sum P(3) = 0.00016 Identities = 9/37 (24%), Positives = 16/37 (43%)

Query: 67 SQPDPNRFDRDRLFNAVSRGVPEDLAGLPEYLSKTSK 103 S+P P R+ ++ V + GL E+ S+ Sbjct: 464 SEPFPGRYGKNSTLQQVKPVINATSRGLVEWSEPLSQ 500

Score = 34 (15.8 bits), Expect = 6.8e-11, Sum P(8) = 6.8e-11 Identities = 8/31 (25%), Positives = 17/31 (54%)

Query: 422 LKAEVGNSMLLTGHILLLLGGIYLLVGQLWY 452 L ++ +L+ ++LI + I+ V L+Y Sbjct: 577 LACDLSPVLLVVDNVLITVTMIFTTVHYLYY 607

>GP:gi|3875319|gnl|FID|e1344970 (Z74030) similar to ankyrin repeats
[Caenorhabditis elegans] >GP:gi|3876480|gnl|PID|e1346172 (Z72508)
similar to ankyrin repeats [Caenorhabditis elegans]
Length = 790

Score = 97 (45.0 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19 Identities = 18/53 (33%), Positives = 32/53 (60%)

Query: 497 LLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGFA 549 + + +++ + LYY R G + +m+ +I DL+RF +IY +FL GF+ Sbjct: 526 MAIISILLVTQHFLYYMRAIPFVGPFVLMVYTIIATDLVRFAMIYSIFLVGFS 578

Score = 89 (41.3 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19 Identities = 19/48 (39%), Positives = 27/48 (56%)

Query: 151 LVNAQCTDDYYRGHSALHIAIEKRSLQCVKLLVENGANVHARACGRFF 198 L+N C + Y G S LH+AI + Q LL+ GA+++ R G FF Sbjct: 189 LINDICVSEEYYGLSPLHLAIVNQDAQFTSLLLRLGADLNQRCYGAFF 236

Score = 62 (28.8 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19 Identities = 13/23 (56%), Positives = 14/23 (60%)

Query: 207 YFGELPLSLAACTKQWDVVSYLL 229

YFGE PLS A C Q D+ LL

Sbjct: 267 YFGEYPLSFAICMGQHDLFRMLL 289

Score = 51 (23.7 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19

Identities = 10/19 (52%), Positives = 13/19 (68%)

Query: 236 ASLQATDSQGNTVLHALVM 254

A+L A D+ GNT LH V+

Sbjct: 293 ANLSAQDTNGNTALHLCVI 311

Score = 49 (22.8 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19

Identities = 11/51 (21%), Positives = 27/51 (52%)

Query: 601 KFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSV 651

+F++ E++ + + + L+ + IL N+LIA+M+ T ++

Sbjct: 626 EFSVLYREMSACDNFWMKWIGKLIFVIFET: SILQFNLLIAMMTRTYETI 676

Score = 43 (20.0 bits), Expect = 1.2e-06, Sum P(5) = 1.2e-06

Identities = 7/27 (25%), Positives = 16/27 (59%)

Query: 163 GHSALHIAIEKRSLQCVKLLVENGANV 189

G++ALH+ + + ++E G N+

Sbjct: 302 GNTALHLCVIHDKMDMLDAVLEAGGNI 328

Score = 39 (18.1 bits), Expect = 5.5e-12, Sum P(7) = 5.5e-12

Identities = 12/56 (21%), Positives = 25/56 (44%)

Query: 461 WISFIDSYFEILFLFQALLKPVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGF 516

W +F+ ++ L AL + + CLA ++ L + +++L T+F

Sbjct: 483 WFNFLKAFPAKLMFKGAFLFIIISIPCRLACSFHEFFLTIDNTMAIISILLVTQHF 538

Score = 38 (17.6 bits), Expect = 1.1e-19, Sim P(7) = 1.1e-19

Identities = 9/18 (50%), Positives = 12/18 (66%)

Query: 289 IRNLQDLTPLKLAAKEGK 306

+ N Q+LT L LAA+ K

Sbjct: 330 LANKQNLTALTLAARLAK 347

Score = 37 (17.2 bits), Expect = 4.7e-18, Sum P(7) = 4.7e-18

Identities = 7/15 (46%), Positives = 9/15 (60%)

Query: 723 DPSGAGVPRTLENPV 737

DP G+ +ENPV

Sbjct: 599 DPMGSEFNNIMENPV 613

Score = 36 (16.7 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19

Identities = 10/47 (21%), Positives = 16/47 (34%)

Query: 376 LNKLLQAKWDLLIPKFFLNFLCNLIYMFIFTAVAYHQPTLKKAAPHL 422

+ ++L KW +L L I+ + AY HL

Sbjct: 362 IEQILDEKWKAYGRALWLRSLLGFIFFYCCFVCAYMLRPSSATTEHL 408

Score = 35 (16.3 bits), Expect = 3.0e-08, 90m P(6) = 3.0e-08

Identities = 9/23 (39%), Positives = 11/23 (47%)

Query: 207 YFGELPLSLAACTKQWDVVSYLL 229

Y+G PL LA + S LL

Sbjct: 199 YYGLSPLHLAIVNQDAQFTSLLL 221

Score = 34 (15.8 bits), Expect = 3.9e-12, Sum P(5) = 3.9e-12

Identities = 7/21 (33%), Positives = 13/21 (61%)

Query: 297 PLKLAAKEGKIEIFRHILQRE 317

PL A G+ ++FR +L ++

Sbjct: 272 PLSFAICMGQHDLFRMLLAKK 292

Score = 34 (15.8 bits), Expect = 8.9e-10, Sum P(7) = 8.9e-10

Identities = 6/18 (33%), Positives = 12/18 (66%)

Query: 610 AFQEQLHFRGMVLLLLLA 627

AF +L F+G L ++++

Sbjct: 489 AFPAKLMFKGAFLFIIIS 506

Score = 34 (15.8 bits), Expect = 4.0e-08, Sum P(6) = 4.0e-08

Identities = 11/40 (27%), Positives = 16/40 (40%)

Query: 153 NAQCTDDYYRGHSALHIAIEKRSLQCVKLLVENGANVHAR 192

N T YG L AI ++L+ AN+ A+

Sbjcc: 259 NTNYTGSMYFGEYPLSFAICMGQHDLFRMLLAKKANLSAQ 298

>GP:gi|2642590 (AF031408) olfactory channel [Caenorhabditis elegans]
Length = 937

Score = 93 (43.2 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16 Identities = 19/36 (52%), Positives = 25/36 (69%)

Query: 163 GHSALHIATEKRSLQCVKLLVENGANVHARACGRFF 198

G SALH+AI + V LL+ + A+V+ARACG FF

Sbjct: 172 GQSALHLAIVHDDYETVSLLLNSKADVNARACGNFF 207

Score = 92 (42.7 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16

Identities = 20/53 (37%), Positives = 31/53 (58%)

Query: 497 LLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGFA 549

L V AL W+ LL++ R + TG + MI +I D++RF +I +FL F+

Sbjct: 500 LFVFALPGSWIFLLFFARSAKLTGPFVQMIYSMIAGDMIRFAIISAIFLVSFS 552

Score = 57 (26.5 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16

Identities = 10/24 (41%), Positives = 15/24 (62%)

Query: 207 YFGELPLSLAACTKQWDVVSYLLE 230

Y+GE PL+ AAC D+ L++

Sbjct: 226 YYGEYPLAFAACFGNKDIYDLLIQ 249

Score = 50 (23.2 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16

Identities = 11/25 (44%), Positives = 15/25 (60%)

Query: 291 NLQDLTPLKLAAKEGKIEIFRHILQ 315

N TPL LAKG+ +IF +L+

Sbjct: 294 NHAGFTPLTLATKLGRKQIFEEMLE 318

Score = 44 (20.4 bits), Expect = 6.8e-16, Sam P(5) = 6.8e-16

Identities = 10/24 (41%), Positives = 15/24 (62%)

Query: 242 DSQGNTVLHALVMISDNSAENIAL 265

DS GNT+LH V+ +S + A+

Sbjct: 258 DSFGNTILHMCVINYSSSMYSYAV 281

Score = 37 (17.2 bits), Expect = 2.2e-05, Sum P(4) = 2.2e-05

Identities = 9/24 (37%), Positives = 13/24 (54%)

Query: 208 FGELPLSLAACTKQWDVVSYLLEN 231

FG+ L LA ++ VS LL +

Sbjct: 171 FGQSALHLAIVHDDYETVSLLLNS 194

Score = 34 (15.8 bits), Expect = 3.6e-16, Sum P(6) = 3.6e-16Identities = 7/21 (33%), Positives = 11/21 (52%)

Query: 364 SPHRHRMVVLEFLNKLLQAKW 384 +P M+ E + +LL KW Sbjct: 363 TPEHLDMIGSEVIQRLLADKW 383

>GP:gi|2854148 (AF045639) contains similarity to ankyrin repeats [Caenorhabditis elegans]

Length = 957

Score = 93 (43.2 bits), Expect = 7.6e-16, Sum F(5) = 7.6e-16Identities = 19/36 (52%), Positives = 25/36 (69%)

Query: 163 GHSALHIAIEKRSLQCVKLLVENGANVHARACGRFF 198
G SALH+AI + V LL+ + A+V+ARACG FF
Sbjct: 175 GQSALHLAIVHDDYETVSLLLNSKADVNARACGNFF 210

Score = 92 (42.7 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16Identities = 20/53 (37%), Positives = 31/53 (58%)

Query: 497 LLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGFA 549 L V AL W+ LL++ R + TG + MI +I D++RF +I +FL F+ Sbjct: 503 LFVFALPGSWIFLLFFARSAKLTGPFVQMIYSMIAGDMIRFAIISAIFLVSFS 555

Score = 57 (26.5 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16 Identities = 10/24 (41%), Positives = 15/24 (62%)

Query: 207 YFGELPLSLAACTKQWDVVSYLLE 230 Y+GE PL+ AAC D+ L++ Sbjct: 229 YYGEYPLAFAACFGNKDIXDLLIQ 252

Score = 50 (23.2 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16Identities = 11/25 (44%), Positives = 15/25 (60%)

Query: 291 NLQDLTPLKLAAKEGKIEIFRHILQ 315 N TPL LA K G+ +IF +L+ Sbjct: 297 NHAGFTPLTLATKLGRKQIFEEMLE 321

Score = 44 (20.4 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16 Identities = 10/24 (41%), Positives = 15/24 (62%)

Query: 242 DSQGNTVLHALVMISDNSAENIAL 265 DS GNT+LH: V+ +S + A+ Sbjct: 261 DSFGNTILHMCVINYSSSMYSYAV 284

Score = 37 (17.2 bits), Expect = 2.4e-05, Sum P(4) = 2.4e-05 Identities = 9/24 (37%), Positives = 13/24 (54%)

Query: 208 FGELPLSLAACTKQWDVVSYLLEN 231
FG+ L LA ++ VS LL +
Sbjct: 174 FGQSALHLAIVHDDYETVSLLLNS 197

Score = 34 (15.8 bits), Expect = 4.1e-16, Sum P(6) = 4.1e-16 Identities = 7/21 (33%), Positives = 11/21 (52%)

Query: 364 SPHRHRMVVLEPLNKLLQAKW 384 +P M+ E + +LL KW Sbjct: 366 TPEHLDMIGSEVIQRLLADKW 386 >GP:gi|3879753|gn1|PID|e1349345 (Z72514) Similarity to Human ankyrin (SW:ANK1_HUMAN) [Caenorhabditis elegans]
Length = 519

Score = 73 (33.9 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11
Identities = 17/36 (47%), Positives = 19/36 (52%)

Query: 163 GHSALHIAIEKRSLQCVKLLVENGANVHARACGRFF 198
G S LH AI L+ V L GA+VH R G FF

Sbjct: 186 GLSPLHQAIVNEDLEMVYFLCRKGADVHQRCYGSFF 221

Score = 63 (29.3 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11 Identities = 12/17 (70%), Positives = 13/17 (76%)

Query: 207 YFGELPLSLAACTKQWD 223 Y+GE PLS AACT Q D Sbjct: 252 YWGEYPLSFAACTNQVD 268

Score = 52 (24.1 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11Identities = 13/27 (48%), Positives = 17/27 (62%)

Query: 289 IRNLQDLTPLKLAAKEGKIEIFRHILQ 315 +RN LTPL LAA+ K I+ IL+ Sbjct: 315 VRNNLKLTPLALAARLAKKHIYDLILE 341

Score = 51 (23.7 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11 Identities = 10/22 (45%), Positives = 12/22 (54%)

Query: 331 WCYGPVRVSLYDLASVDSCEEN 352 W YGPV Y L VD+ E+ Sbjct: 348 WRYGPVVCKAYPLNDVDTINES 369

Score = 43 (20.0 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11 Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 242 DSQGNTVLHALVM 254 D+ GNTVLH V+ Sbjct: 284 DTNGNTVLHLTVI 296

Score = 37 (17.2 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11Identities = 8/35 (22%), Positives = 16/35 (45%)

Query: 376 LNKLLQAKWDLLIPKFFLNFLCNLIYMFIF® VAY 410 + ++L+KW+ K L IY +A+ Sbjct: 398 IEEVLESKWETFGKKQLFMSLAGYIYFLAVFYLAF 432

>GP:gi|3287188|gml|PID|e315126 (Y10601) ankyrin-like protein [Homo sapiens]
Length = 1119

Score = 71 (33.0 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08 Identities = 13/30 (43%), Positives = 20/30 (66%)

Query: 163 GHSALHIAIEKRSLQCVKLLVENGANVHAR 192 G++ LH A+EK ++ VK L+ GAN + R Sbjct: 98 GNTPLHCAVEKNQIESVKFLLSRGANPNLR 127

Score = 63 (29.3 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08Identities = 10/30 (33%), Positives = 20/30 (66%)

Query: 501 ALVLGWLNLLYYTRGFQHTGIYSVMIQKVI 530 A+ W+N L Y + F++ GI+ VM++ ++ Sbjct: 838 AVYFYWMNFLLYLQRFENCGIFIVMLEVIL 467 Score = 59 (27.4 bits), Expect = 9.0e-07, Som P(6) = 9.0e-07 Identities = 10/30 (33%), Positives = 19/30 (63%)

Query: 167 LHIAIEKRSLQCVKLLVENGANVHARACGR 196 LH+A++ L+ +K+ ++NGA + GR Sbjct: 243 LHLAVQNGDLEMIKMCLDNGAQIDPVEKGR 272

Score = 50 (23.2 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08Identities = 10/26 (38%), Positives = 18/26 (69%)

Query: 291 NLQDLTFLKLAAKEGKIEIFRHILQR 316 +L +TPL LAAK G ++ + +L++ Sbjct: 479 DLHGMTPLHLAAKNGHDKVVQLLLKK 504

Score = 49 (22.8 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08 Identities = 10/26 (38%), Positives = 14/26 (53%)

Query: 209 GELPLSLAACTKQWDVVSYLLENPHQ 234
G PL LA + W++V+ LL Q
Sbjct: 342 GRSPLILATASASWNIVNLLLSKGAQ 367

Score = 48 (22.3 bits), Expect = 3.2e-05, Sum P(5) = 3.2e-05Identities = 9/32 (28%), Positives = 20/32 (62%)

Query: 524 VMIQKVILRDLLRFLLIYLVFLFGFAVALVSL 555 +++ +VIL+ LLR ++++ L F ++ L Sbjct: 860 IVMLEVILKTLLRSTVVFIFLLLAFGLSFYIL 891

Score = 41 (19.0 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08 Identities = 9/28 (32%), Positives = 15/28 (53%)

Query: 525 MIQKVILRDLLRFLLIYLVFLFGFAVAL 552 +I K +LR + F+ + L F F + L Sbjct: 865 VILKTLLRSTVVFIFLLLAFGLSFYILL 892

Score = 40 (18.6 bits), Expect = 2.9e-07, Sum P(5) = 2.9e-07Identities = 13/50 (26%), Positives = 24/50 (48%)

Query: 620 MVLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSIWKLQKAISVLE 669 +V + LL L++ +LLN+ S ++ ÷ T S + + S LE Sbjct: 875 VVFIFLLLAFGLSFYILLNLQDPFSSPLLSIIQTFSMMLGDINYRESFLE 924

Score = 40 (18.6 bits), Expect = 7.6e-05, Sum P(5) = 7.6e-05Identities = 8/19 (42%), Positives = 12/19 (63%)

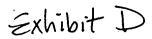
Query: 296 TPLKLAAKEGKIEIFRHIL 314 TPL LA + G +E+ + L Sbjet: 241 TPLHLAVQNGDLEMIKMCL 259

Score = 39 (18.1 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08 Identities = 7/19 (36%), Positives = 14/19 (73%)

Query: 625 LLAYVLLTYILLINMLIAL 643 L+++ + I+L+N+LI L Sbjct: 941 LVSFTIFVPIVLMNLLIGL 959

Score = 39 (18.1 bits), Expect = 6.8e-07, Sum P(6) = 6.8e-07Identities = 9/36 (25%), Positives = 18/36 (50%)

Query: 293 QDLTPLKLAAKEGKIEIFRHILQREFSGLSHLSRKF 328 + LT L '+ +IE+ H + +E+ + L+ F Sbjet: 681 EPLTALNAMVQNNRIELLNHPVCKEYLLMKWLAYGF 716





Qualified Target Summary Sheet

	Vanilloid Receptor Homologue
	(VR-2)
CFA Disease Area (s):	Pain
Druggable Target Class:	Calcium channel
MPI Gene Sequence Identifier:	Flh21e11 (Mine 18560)
Top Blast Hit:	Rat vanilloid receptor 1 (VR1)
Amino Acid Coding Region:	ORF: 361-2652
CDNA Length:	2806 bp
Source (Tissue / Cell Line):	First clone identified in an internal heart library
Novel / Unrecognized:	? Unrecognized / Novel
% Novelty:	66% novel across the complete cDNA. Hits unannotated sequence in Non-Public Patent Data Base
Patent Status:	Filed Nov. 1, 1998
Full Length Clone:	Yes
Expression Profiling Results:	Present in a sub-population of sensory neurons different from VR1. Also present in sympathetic neurons.
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Background:	The published vanilloid receptor (Caterina et. Al. Nature 389:816-24, 1997) responds to heat and capsaicin by activating Ca++ influx in sensory neurons (Tominaga et.al., Neuron 21: 531-43, 1998). Capsaicin also binds to this channel.
Hypothesis:	This channel may be responsible for hypersensitivity in chronic neuropathic pain and represents a unique target for pain.
Assay Type:	Cell-based assay
Reagents Needed:	Open reading frame will be cloned by Millennium into pCDNA 3.1
Readout:	
Critical Experiments Necessary:	

MPI Target Name:

Vanilloid Receptor Homologue (VR-2)

QT Nomination Date:

12/22/98

Acti n Tak n:

Date Accepted: Bay r QT Leader: Accepted QT (unrecognized) Pending full length cDNA

MPI QT Leader:

Rory Curtis or Peter DiStefano